

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

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Protein Sequence (21 letters)

Results for: None(21aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|55601

Description

None

Molecule type

amino acid

Query Length

21

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Related Structures\]](#) [\[Multiple alignment\]](#) [\[NEW\]](#)

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date Dec 10, 2009 5:41 PM
Number of letters 3,463,213,929
Number of sequences 10,157,076

Entrez query none

Karlin-Altschul statistics

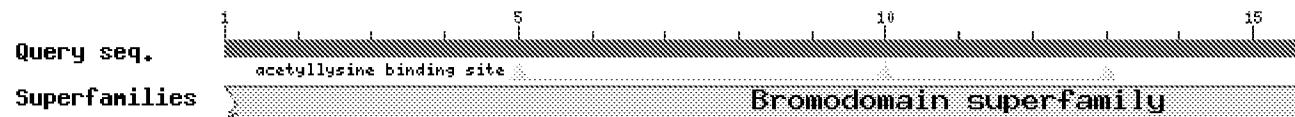
Params	Ungapped	Gapped
Lambda	0.332117	0.294
K	0.27808	0.11
H	1.83624	0.61

Results Statistics

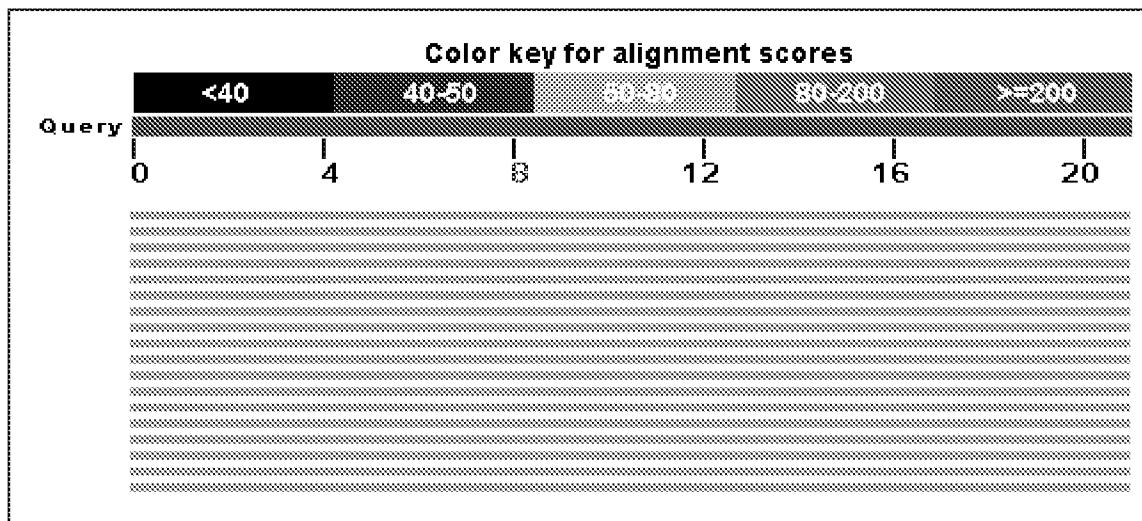
Length adjustment	11
Effective length of query	10
Effective length of database	3351486093
Effective search space	33514860930
Effective search space used	33514860930

[Graphic Summary](#)[Show Conserved Domains](#)

Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 104 Blast Hits on the Query Sequence**[\[?\]](#)

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

		Score
E	Sequences producing significant alignments:	(Bits) Value
ref XP_002194393.1	PREDICTED: p300/CBP-associated factor [Ta...	69.8 3e-11
ref XP_001493774.2	PREDICTED: p300/CBP-associated factor [Eq...	69.8 3e-11
ref XP_001508358.1	PREDICTED: similar to PCAF [Ornithorhynch...	69.8 3e-11
gb EDL82853.1	p300/CBP-associated factor, isoform CRA_b [Rat...	69.8 3e-11
gb EDL82852.1	p300/CBP-associated factor, isoform CRA_a [Rat...	69.8 3e-11
gb EDL23666.1	p300/CBP-associated factor, isoform CRA_b [Mus...	69.8 3e-11
gb EDL23665.1	p300/CBP-associated factor, isoform CRA_a [Mus...	69.8 3e-11
ref XP_001380514.1	PREDICTED: similar to p300/CBP-associated...	69.8 3e-11
ref XP_613744.3	PREDICTED: p300/CBP-associated factor [Bos t...	69.8 3e-11
gb EAW64305.1	p300/CBP-associated factor, isoform CRA_a [Hom...	69.8 3e-11
gb EAW64306.1	p300/CBP-associated factor, isoform CRA_b [Hom...	69.8 3e-11
ref XP_426001.2	PREDICTED: similar to PCAF [Gallus gallus]	69.8 3e-11
ref XP_516321.2	PREDICTED: p300/CBP-associated factor [Pan t...	69.8 3e-11
ref XP_001086307.1	PREDICTED: similar to p300/CBP-associated...	69.8 3e-11
dbj EAE59136.1	PCAF [Gallus gallus]	69.8 3e-11
gb AAC50890.2	p300/CBP-associated factor [Homo sapiens]	69.8 3e-11
gb AAF70498.1 AF254442.1	PCAF acetyltransferase [Mus musculus]	69.8 3e-11
ref XP_534249.2	PREDICTED: similar to p300/CBP-associated fa...	69.8 3e-11
ref NP_064389.2	K(lysine) acetyltransferase 2B [Mus musculus...]	69.8 3e-11
ref NP_003875.3	K(lysine) acetyltransferase 2B [Homo sapiens...]	69.8 3e-11
dbj EAE33658.1	unnamed protein product [Mus musculus]	69.8 3e-11
pdb 1N72 A	Chain A, Structure And Ligand Of A Histone Acetyl...	69.8 3e-11
ref NP_001019423.1	K(lysine) acetyltransferase 2B [Rattus no...	66.0 5e-10
gb EDL05223.1	mCG4405 [Mus musculus]	65.5 6e-10
ref XP_911230.1	PREDICTED: similar to P300/CBP-associated fa...	65.5 6e-10
ref XP_284106.1	PREDICTED: similar to P300/CBP-associated fa...	65.5 6e-10
ref NP_001038499.1	K(lysine) acetyltransferase 2B [Danio rer...	59.6 4e-08
emb CAF99403.1	unnamed protein product [Tetraodon nigroviridis]	59.6 4e-08
pdb 3D7C A	Chain A, Crystal Structure Of The Bromodomain Of H...	54.9 1e-06
ref XP_001495139.2	PREDICTED: similar to GCN5 general contro...	54.9 1e-06
ref XP_001922732.1	PREDICTED: im:7156024 [Danio rerio]	54.9 1e-06
gb EDL02540.1	GCN5 general control of amino acid synthesis-1...	54.9 1e-06
gb EDL02538.1	GCN5 general control of amino acid synthesis-1...	54.9 1e-06
gb EAW60801.1	GCN5 general control of amino-acid synthesis 5...	54.9 1e-06
gb EAW60802.1	GCN5 general control of amino-acid synthesis 5...	54.9 1e-06
ref XP_511500.2	PREDICTED: GCN5 general control of amino-aci...	54.9 1e-06
ref XP_001166738.1	PREDICTED: GCN5 general control of amino-...	54.9 1e-06
ref NP_001100520.1	general control of amino acid synthesis 5...	54.9 1e-06
ref XP_001094333.1	PREDICTED: similar to GCN5 general contro...	54.9 1e-06
gb AAQ03834.1	general control of amino-acid synthesis 5-like...	54.9 1e-06
gb AAK03983.1	Kat2a protein [Mus musculus]	54.9 1e-06
pdb 1F68 A	Chain A, Nmr Solution Structure Of The Bromodomain...	54.9 1e-06
gb AAC50641.1	GCN5 [Homo sapiens]	54.9 1e-06

ref XP_860469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_860436.1	PREDICTED: similar to General control of ami...	54.9	1e-06
ref XP_860364.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_860401.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_849978.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_548094.2	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
gb AAC50690.1	hGCN5=transcriptional adaptor [human, testis, ...	54.9	1e-06
ref NP_066564.2	general control of amino acid synthesis 5-li...	54.9	1e-06
dbj BAE29392.1	unnamed protein product [Mus musculus]	54.9	1e-06
dbj BAE26296.1	unnamed protein product [Mus musculus]	54.9	1e-06
dbj BAE33207.1	unnamed protein product [Mus musculus]	54.9	1e-06
ref NP_064388.2	general control of amino acid synthesis 5-li...	54.9	1e-06
ref NP_001033099.1	general control of amino acid synthesis 5...	54.9	1e-06
SP Q3JRD2.1 KAT2A_MOUSE	RecName: Full=Histone acetyltransfera...	54.9	1e-06
gb AAC39769.1	hGCN5 [Homo sapiens]	54.9	1e-06
ref XP_001515022.1	PREDICTED: similar to GCN5 general contro...	54.8	1e-06
ref XP_002194616.1	PREDICTED: GCN5 general control of amino-...	52.8	4e-06
gb CAG02829.1	unnamed protein product [Tetraodon nigroviridis]	52.8	4e-06
ref NP_989660.1	general control of amino acid synthesis 5-li...	52.8	4e-06
ref XP_002123196.1	PREDICTED: similar to K(lysine) acetyltra...	51.1	1e-05
dbj EFAL0157.1	hypothetical protein TcasGA2_TC012345 [Triboli...	48.6	8e-05
ref XP_002427469.1	fetal alzheimer antigen, falz, putative [...]	48.6	8e-05
ref XP_001811424.1	PREDICTED: similar to fetal alzheimer ant...	48.6	8e-05
ref XP_001983459.1	GH14490 [Drosophila grimshawi] >gb EDV978...	46.0	5e-04
ref XP_001605087.1	PREDICTED: similar to fetal alzheimer ant...	44.8	0.001
ref XP_395718.3	PREDICTED: similar to Enhancer of bithorax C...	44.8	0.001
ref XP_002092980.1	GE21036 [Drosophila yakuba] >gb EDW92692....	44.3	0.002
ref XP_001970994.1	GG14675 [Drosophila erecta] >gb EDV50020....	44.3	0.002
gb AAL16644.1 AF417921.1	nucleosome remodeling factor large s...	44.3	0.002
ref NP_728505.1	enhancer of bithorax, isoform B [Drosophila ...	44.3	0.002
ref NP_728507.1	enhancer of bithorax, isoform A [Drosophila ...	44.3	0.002
ref XP_002117619.1	predicted protein [Trichoplax adhaerens] ...	43.9	0.002
ref XP_002341863.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002341882.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002151156.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002151155.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_001352486.2	GA16840 [Drosophila pseudoobscura pseudoo...	43.5	0.003
ref XP_002026084.1	GL16133 [Drosophila persimilis] >gb EDW33...	43.5	0.003
ref XP_001956111.1	GF24755 [Drosophila ananassae] >gb EDV389...	43.5	0.003
ref XP_002062665.1	GK17657 [Drosophila willistoni] >gb EDW73...	43.1	0.004
ref XP_002060306.1	GJ16047 [Drosophila virilis] >gb EDW57119...	43.1	0.004
ref XP_001983171.1	GH15750 [Drosophila grimshawi] >gb EDV955...	43.1	0.004
ref XP_002627606.1	histone acetyltransferase GCN5 [Ajellomyc...	42.6	0.005
ref XP_316196.4	AGAP006133-PA [Anopheles gambiae str. PEST] ...	42.6	0.005
ref XP_002383268.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001389241.1	hypothetical protein An01g08160 [Aspergil...	42.2	0.007
ref XP_001266775.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001272118.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007

ref XP_001212327.1	histone acetyltransferase GCN5 [Aspergill...	42.2	0.007
ref XP_001816805.1	hypothetical protein [Aspergillus oryzae ...	42.2	0.007
ref XP_751566.1	histone acetyltransferase (Gcn5) [Aspergillu...	42.2	0.007
gb EEB24293.1	histone acetyltransferase GCN5, putative [Cocc...	41.8	0.009
ref XP_002541088.1	histone acetyltransferase GCN5 [Uncinocar...	41.8	0.009
gb EEB45435.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEB36638.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEB20829.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009

Alignments Select All Get selected sequences Distance tree of results Multiple alignment [NEW](#)

>**pdb|3GG3|A** Chain A, Crystal Structure Of The Bromodomain Of Human Pcaf
pdb|3GG3|B Chain B, Crystal Structure Of The Bromodomain Of Human Pcaf
Length=119

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 36 FMEPVKRTEAPGYYEVIRFPM 56

>**ref|XP_002194393.1|** PREDICTED: p300/CBP-associated factor [Taeniopygia guttata]
Length=742

GENE ID: 100227387 LOC100227387 | p300/CBP-associated factor [Taeniopygia guttata]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 658 FMEPVKRTEAPGYYEVIRFPM 678

>**ref|XP_001493774.2|** PREDICTED: p300/CBP-associated factor [Equus caballus]
Length=784

GENE ID: 100061976 KAT2B | K(lysine) acetyltransferase 2B [Equus caballus]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 700 FMEPVKRTEAPGYYEVIRFPM 720

>**ref|XP_001508358.1|** PREDICTED: similar to PCAF [Ornithorhynchus anatinus]
Length=817

GENE ID: 100077074 LOC100077074 | similar to PCAF [Ornithorhynchus anatinus]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 733 FMEPVKRTEAPGYYEVIRFPM 753

>**gb|EDL82853.1|** p300/CBP-associated factor, isoform CRA_b [Rattus norvegicus]
Length=704

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 620 FMEPVKRTEAPGYYEVIRFPM 640

>**gb|EDL82852.1|** p300/CBP-associated factor, isoform CRA_a [Rattus norvegicus]
 Length=731

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 647 FMEPVKRTEAPGYYEVIRFPM 667

>**gb|EDL23666.1|** p300/CBP-associated factor, isoform CRA_b [Mus musculus]
 Length=706

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
 (Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 622 FMEPVKRTEAPGYYEVIRFPM 642

>**gb|EDL23665.1|** p300/CBP-associated factor, isoform CRA_a [Mus musculus]
 Length=746

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
 (Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 662 FMEPVKRTEAPGYYEVIRFPM 682

>**ref|XP_001380514.1|** PREDICTED: similar to p300/CBP-associated factor, [Mono
 domestica]
 Length=966

GENE ID: 100031193 LOC100031193 | similar to p300/CBP-associated factor
 [Monodelphis domestica]

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 882 FMEPVKRTEAPGYYEVIRFPM 902

>**ref|XP_613744.3|** PREDICTED: p300/CBP-associated factor [Bos taurus]
 Length=826

GENE ID: 407215 KAT2B | K(lysine) acetyltransferase 2B [Bos taurus]

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM

Sbjct 742 FMEPVKRTEAPGYYEVIRFPM 762

>gb|EAW64305.1|  p300/CBP-associated factor, isoform CRA_a [Homo sapiens]
Length=825

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

 Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

 Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 741 FMEPVKRTEAPGYYEVIRFPM 761

>gb|EAW64306.1|  p300/CBP-associated factor, isoform CRA_b [Homo sapiens]
Length=768

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

 Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

 Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 741 FMEPVKRTEAPGYYEVIRFPM 761

>ref|XP_426001.2|  PREDICTED: similar to PCAF [Gallus gallus]
Length=753

GENE ID: 428441 PCAF | p300/CBP-associated factor [Gallus gallus]
(10 or fewer PubMed links)

 Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

 Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 669 FMEPVKRTEAPGYYEVIRFPM 689

>ref|XP_516321.2|  PREDICTED: p300/CBP-associated factor [Pan troglodytes]
Length=806

GENE ID: 460219 KAT2B | K(lysine) acetyltransferase 2B [Pan troglodytes]

 Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

 Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 722 FMEPVKRTEAPGYYEVIRFPM 742

>ref|XP_001086807.1|  PREDICTED: similar to p300/CBP-associated factor [Macac
Length=858

GENE ID: 698283 LOC698283 | similar to p300/CBP-associated factor
[Macaca mulatta]

 Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

 Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVKRTEAPGYYEVIR PM
 Sbjct 774 FMEPVKRTEAPGYYEVIRFPM 794

>dbj|BAB59138.1|  PCAF [Gallus gallus]
Length=760

GENE ID: 428441 PCAF | p300/CBP-associated factor [Gallus gallus]
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 676 FMEPVKRTEAPGYYEVIRFPM 696

>**gb|AAC50890.2|** p300/CBP-associated factor [Homo sapiens]
Length=832

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 748 FMEPVKRTEAPGYYEVIRFPM 768

>**gb|AAF70498.1|AF254442_1|** PCAF acetyltransferase [Mus musculus]
Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 729 FMEPVKRTEAPGYYEVIRFPM 749

>**ref|XP_534249.2|** PREDICTED: similar to p300/CBP-associated factor [Canis fa
Length=760

GENE ID: 477052 KAT2B | K(lysine) acetyltransferase 2B [Canis lupus familiaris]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 676 FMEPVKRTEAPGYYEVIRFPM 696

>**ref|NP_064389.2|** K(lysine) acetyltransferase 2B [Mus musculus]

sp|Q9JHD1.2|KAT2B_MOUSE RecName: Full=Histone acetyltransferase KAT2B; AltName=acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF

gb|AAH82581.1| K(lysine) acetyltransferase 2B [Mus musculus]

gb|EDL23667.1| p300/CBP-associated factor, isoform CRA_c [Mus musculus]

gb|AAI45897.1| K(lysine) acetyltransferase 2B [Mus musculus]

gb|AAI38196.1| K(lysine) acetyltransferase 2B [Mus musculus]
Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 729 FMEPVKRTEAPGYYEVIRFPM 749

>**ref|NP_003875.3|** K(lysine) acetyltransferase 2B [Homo sapiens]
sp|Q92831.3|KAT2B_HUMAN RecName: Full=Histone acetyltransferase KAT2B; AltName acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF
gb|AAH60823.1| K(lysine) acetyltransferase 2B [Homo sapiens]
gb|AAH70075.1| K(lysine) acetyltransferase 2B [Homo sapiens]
dbj|BAI45566.1| K(lysine) acetyltransferase 2B [synthetic construct]
Length=832

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 748 FMEPVKRTEAPGYYEVIRFPM 768

>**dbj|BAE33658.1|** unnamed protein product [Mus musculus]
Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 729 FMEPVKRTEAPGYYEVIRFPM 749

>**pdb|1N72|A** Chain A, Structure And Ligand Of A Histone Acetyltransferase Bromodomain

pdb|1JM4|B Chain B, Nmr Structure Of PCAF BROMODOMAIN IN COMPLEX WITH HIV-1 Tat Peptide

pdb|1WUG|A Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np1

pdb|1WUM|A Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np2

pdb|1ZS5|A Chain A, Structure-Based Evaluation Of Selective And Non-Selecti Small Molecules That Block Hiv-1 Tat And Pcaf Association

pdb|2RNW|A Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp

pdb|2RNX|A Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp
Length=118

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
FMEPVKRTEAPGYYEVIR PM
Sbjct 34 FMEPVKRTEAPGYYEVIRFPM 54

>**ref|NP_001019423.1|** K(lysine) acetyltransferase 2B [Rattus norvegicus]

gb|AAH92639.1| P300/CBP-associated factor [Rattus norvegicus]
Length=84

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 66.0 bits (148), Expect = 5e-10

Identities = 19/20 (95%), Positives = 19/20 (95%), Gaps = 0/20 (0%)

Query 2 MEPVKRTEAPGYYEVIRSPM 21
 MEPVKRTEAPGYYEVIR PM
 Sbjct 1 MEPVKRTEAPGYYEVIRFPM 20

>**gb|EDL05223.1|** mCG4405 [Mus musculus]
 Length=813

Score = 65.5 bits (147), Expect = 6e-10
 Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 F+EPVKRTEAPGYYEVIR PM
 Sbjct 729 FLEPVKRTEAPGYYEVIRFPM 749

>**ref|XP_911230.1|** PREDICTED: similar to P300/CBP-associated factor [Mus musculus]
 Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10
 Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 F+EPVKRTEAPGYYEVIR PM
 Sbjct 745 FLEPVKRTEAPGYYEVIRFPM 765

>**ref|XP_284106.1|** PREDICTED: similar to P300/CBP-associated factor [Mus musculus]
 Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10
 Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 F+EPVKRTEAPGYYEVIR PM
 Sbjct 745 FLEPVKRTEAPGYYEVIRFPM 765

>**ref|NP_001038499.1|** K(lysine) acetyltransferase 2B [Danio rerio]

emb|CAK04378.1| novel protein similar to vertebrate p300/CBP-associated factor (PCAF) [Danio rerio]
 Length=796

GENE ID: 563942 kat2b | K(lysine) acetyltransferase 2B [Danio rerio]
 (10 or fewer PubMed links)

Score = 59.6 bits (133), Expect = 4e-08
 Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVK+ EAPGYY+VIR PM
 Sbjct 712 FMEPVKKNEAPGYYQVIRFPM 732

>**emb|CAF99403.1|** unnamed protein product [Tetraodon nigroviridis]
 Length=701

Score = 59.6 bits (133), Expect = 4e-08
 Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSPM 21
 FMEPVK+TEAPGYY+ IR PM
 Sbjct 617 FMEPVKKTEAPGYYQAIRFPM 637

>**pdb|3D7C|A** Chain A, Crystal Structure Of The Bromodomain Of Human Gcn5, The General Control Of Amino-Acid Synthesis Protein 5-Like 2

pdb|3D7C|B Chain B, Crystal Structure Of The Bromodomain Of Human Gcn5, The General Control Of Amino-Acid Synthesis Protein 5-Like 2

Length=112

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 28 FMEPVKKSEAPDYYEVIRFP 47

>**ref|XP_001495139.2|**  PREDICTED: similar to GCN5 general control of amino-acid 5-like 2 [Equus caballus]
 Length=836

GENE ID: 100053057 LOC100053057 | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Equus caballus]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 752 FMEPVKKSEAPDYYEVIRFP 771

>**ref|XP_001922732.1|**  PREDICTED: im:7156024 [Danio rerio]
 Length=795

GENE ID: 555517 kat2a | K(lysine) acetyltransferase 2A [Danio rerio]
 (10 or fewer PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 711 FMEPVKKSEAPDYYEVIRFP 730

>**gb|EDL02540.1|**  GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA_C [Mus musculus]
 Length=481

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 397 FMEPVKKSEAPDYYEVIRFP 416

>**gb|EDL02538.1|**  GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA_a [Mus musculus]
 Length=845

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 761 FMEPVKKSEAPDYYEVIRFP 780

>**gb|EAW60801.1|**  GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA_a [Homo sapiens]
 Length=477

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 393 FMEPVKKSEAPDYYEVIRFP 412

>**gb|EAW60802.1|**  GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA_b [Homo sapiens]
 Length=838

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 754 FMEPVKKSEAPDYYEVIRFP 773

>**ref|XP_511500.2|**  PREDICTED: GCN5 general control of amino-acid synthesis 5-2 isoform 2 [Pan troglodytes]
 Length=837

GENE ID: 454677 KAT2A | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 753 FMEPVKKSEAPDYYEVIRFP 772

>**ref|XP_001166738.1|**  PREDICTED: GCN5 general control of amino-acid synthesis 2 isoform 1 [Pan troglodytes]
 Length=852

GENE ID: 454677 KAT2A | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 768 FMEPVKKSEAPDYYEVIRFP 787

>**ref|NP_001100520.1|**  general control of amino acid synthesis 5-like 2 [Rattus
gb|EDM06059.1|  GCN5 general control of amino acid synthesis-like 2 (yeast) (p [Rattus norvegicus]
 Length=832

GENE ID: 303539 Gcn5l2 | GCN5 general control of amino acid synthesis-like 2 (yeast) [Rattus norvegicus]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 748 FMEPVKKSEAPDYYEVIRFP 767

>**ref|XP_001094333.1|**  PREDICTED: similar to GCN5 general control of amino-acid 5-like 2 [Macaca mulatta]
 Length=608

GENE ID: 706004 LOC706004 | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Macaca mulatta]

Score = 54.9 bits (122), Expect = 1e-06

Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 524 FMEPVKKSEAPDYYEVIRFP 543

>gb|AAR03834.1| general control of amino-acid synthesis 5-like 2 [Sus scrofa]
 Length=117

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 33 FMEPVKKSEAPDYYEVIRFP 52

>gb|AAH03983.1|  Kat2a protein [Mus musculus]
 Length=116

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 32 FMEPVKKSEAPDYYEVIRFP 51

>pdb|1F68|A  Chain A, Nmr Solution Structure Of The Bromodomain From Human Gcn5
 Length=103

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 24 FMEPVKKSEAPDYYEVIRFP 43

>gb|AAC50641.1|  GCN5 [Homo sapiens]
 Length=476

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
 (Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 392 FMEPVKKSEAPDYYEVIRFP 411

>ref|XP_860469.1|  PREDICTED: similar to GCN5 general control of amino-acid s 5-like 2 isoform 7 [Canis familiaris]
 Length=831

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 747 FMEPVKKSEAPDYYEVIRFP 766

>ref|XP_860436.1|  PREDICTED: similar to General control of amino acid synthe protein 5-like 2 (Histone acetyltransferase GCN5) (mmGCN5) isoform 6 [Canis familiaris]
 Length=843

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 759 FMEPVKKSEAPDYYEVIRFP 778

>**ref|XP_860364.11|**  PREDICTED: similar to GCN5 general control of amino-acid s 5-like 2 isoform 4 [Canis familiaris]
 Length=584

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 500 FMEPVKKSEAPDYYEVIRFP 519

>**ref|XP_860401.11|**  PREDICTED: similar to GCN5 general control of amino-acid syn 5-like 2 isoform 5 [Canis familiaris]
 Length=834

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 750 FMEPVKKSEAPDYYEVIRFP 769

>**ref|XP_849978.11|**  PREDICTED: similar to GCN5 general control of amino-acid s 5-like 2 isoform 2 [Canis familiaris]
 Length=844

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 760 FMEPVKKSEAPDYYEVIRFP 779

>**ref|XP_548094.21|**  PREDICTED: similar to GCN5 general control of amino-acid s 5-like 2 isoform 1 [Canis familiaris]
 Length=837

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 753 FMEPVKKSEAPDYYEVIRFP 772

>**gb|AAB50690.1|** hGCN5=transcriptional adaptor [human, testis, Peptide, 427 aa]
 Length=427

Score = 54.9 bits (122), Expect = 1e-06
 Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYYEVIRSP 20
 FMEPVK++EAP YYEVIR P
 Sbjct 343 FMEPVKKSEAPDYYEVIRFP 362